

Figure 10: Alignments of the genes proposed to be used in reassembly

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1
SEQ ID NO:114 (1) ----AANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEHGITAVWI PPAYKGTS-QADVGYGAYDLYDLGEFHQKGTVR
SEQ ID NO:128 (1) -QANTAPVNGTMMQYFEWDL PNDGTLWTKVNKNEASSLSLGIT ALWLPPAYKGTS-QGDVGYGVYDLYDLGEFNQKGTIR
SEQ ID NO:116 (1) AKYSELEQGGVIMQAFYWDVPEGGIWWD TIRQKIP EWYDAGISAIWI PPASKGMGGAYS MGYPDYDFDLGEF YQKGTVE

81
SEQ ID NO:114 (76) TKYGTKGELQSAIKSLHSRDIN VYGDVV INHKG GADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYSDFK
SEQ ID NO:128 (79) TKYGTKTQYLQAIQA AKSAGMQVYADVFNH KAGADSTEWDAVEVNPSNRNQETSGTYQIQAWTKFDFPGRGNTYSSFK
SEQ ID NO:116 (81) TRFGSKEELVNMISTAHQYGIKV IADIVINHRAGGDLEWNPYVGDYTWDFSKVASGKYKAHYMDFHFN-----

161
SEQ ID NO:114 (156) WHWYHFDGTDWDES RKLNR IYKFQG--KAWDWEVSNENGN DYLMYADIDYDHPDVA AEIKRWGTWYANELQLDGFRLDA
SEQ ID NO:128 (159) WRWYHFDGTDWDES RKLNR IYKFRGTGKAWDWEVD TENGNYDYLMFADLDMDHPEVVTELKNWGTWYVNTTNVDGFR LDA
SEQ ID NO:116 (150) ----NYSTSDEGTFGGFPDIDHLVFPFNQYWLWASNES-----YAA YLRSIGIDAWRFDY

241
SEQ ID NO:114 (234) VKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNH SVFDVPLHYQFHAASTQGGGYDMRKL LNG--
SEQ ID NO:128 (239) VKHIKYSFFPDWLTHVRSQTRKNLFAVG EFWSYDVNKLHNYITKTSGMTSLFDAPLHNNFYTASKSSGYFDMRYLLNN--
SEQ ID NO:116 (200) VKGYGAWVVKDWLSQWGG-----WAVGEYWD TNVDALLNWAYSSG--AKVFD FPLYKMD EAFDNKNIPALVYAIQNGE

321
SEQ ID NO:114 (312) TVVSKHPLKAVTFVDNHDTQPGQSLESTVQTWFKPLAYAFIL TRESGYPQVIFYGDMYGTKGDSQ--REIPALKHKIEPIL
SEQ ID NO:128 (317) TLMKDQPSLAVTLVDNHDTQPGQSLQSWVEPWFKPLAYAFIL TRQEGYPCVFYGDYYGIPKYN-----IPGLKSKIDPLL
SEQ ID NO:116 (272) TVVSRDPFKAVTFVANHDTN-----IIWNKYPAYAFILTYE-GQPVI FYRDYEEWLNKD-----KLN NL---I

401
SEQ ID NO:114 (390) KARKQYAYGAQH DYFDHHDIVGW TREGDSSVANSGLAALITDGP GGA KRM YVGRQNAGETWHDITGNRS--EPVVINSEG
SEQ ID NO:128 (392) IARRDYAYGTQRDYIDHQDIIGW TREGIDSKPNSGLAALITDGP GGS KWMYVGKKHAGKVFYDLTGNRS--DTVTINADG
SEQ ID NO:116 (331) WIHEHLAGGSTKILYYDDDELIFMREGY GDRPGL-ITYINLGS DWAERWVN VGSKFAGYTIHEYTG NLGGWVD RYVQYDG

481
SEQ ID NO:114 (468) WGEFHVN-----GGSVSIYVQR-----
SEQ ID NO:128 (470) WGEFKVN-----GGSVSIWVAKTSQVTF TVNNATTISGQNVYVVGNIPELGNWNTANA I KMT PSSYPTWKATIALP
SEQ ID NO:116 (410) WVKLTA PHDPANGYYGYSVWSYAGVG-----

561
SEQ ID NO:114 (485) -----
SEQ ID NO:128 (541) QGKAIEFKFIKKDQSGNVVWESIPNRTYTV PFLSTGSYTASWNVP
SEQ ID NO:116 (437) -----
605

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Figure 12: A graph of the pH rate profiles for 2 different amylases.

